

SEQUENCE LISTING

<110> Xu, Wenfeng
Lofton-Day, Catherine E.
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Presnell, Scott R.
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Novak, Julia E.
Foster, Donald C.
Yee, David P.

<120> UMLR POLYPEPTIDES

<130> 99-75

<150> US 60/160,880

<151> 1999-10-22

<150> US 60/163,215

<151> 1999-11-02

<150> US 60/218,769

<151> 2000-07-17

<150> US 60/222,221

<151> 2000-08-01

<160> 50

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<211> 1162

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (104)...(913)

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gtg ttt acc ctg gcc ttc ctg ggg ctc ttc ttc ctc tac tgc aag cag 595
Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu Tyr Cys Lys Gln
150 155 160

姓名	性别	年龄	籍贯	职业	文化程度	健康状况	婚姻状况	子女情况	其他
王德胜	男	45	山东	农民	小学	良好	已婚	2子1女	
李秀英	女	42	河北	工人	初中	良好	已婚	1子1女	
张国强	男	38	河南	干部	高中	良好	已婚	2子1女	
刘小红	女	35	江苏	教师	大学	良好	已婚	1子1女	
陈为民	男	50	浙江	商人	小学	良好	已婚	3子1女	
赵大刚	男	48	安徽	农民	小学	良好	已婚	2子1女	
孙丽娟	女	40	湖北	工人	初中	良好	已婚	1子1女	
周建民	男	32	湖南	干部	高中	良好	已婚	2子1女	
吴小芳	女	28	江西	教师	大学	良好	已婚	1子1女	
郑为民	男	55	四川	商人	小学	良好	已婚	3子1女	
冯大刚	男	43	广东	农民	小学	良好	已婚	2子1女	
李秀英	女	38	广西	工人	初中	良好	已婚	1子1女	
张国强	男	30	福建	干部	高中	良好	已婚	2子1女	
刘小红	女	25	贵州	教师	大学	良好	已婚	1子1女	
陈为民	男	52	云南	商人	小学	良好	已婚	3子1女	
赵大刚	男	40	陕西	农民	小学	良好	已婚	2子1女	
孙丽娟	女	35	甘肃	工人	初中	良好	已婚	1子1女	
周建民	男	28	宁夏	干部	高中	良好	已婚	2子1女	
吴小芳	女	22	青海	教师	大学	良好	已婚	1子1女	
郑为民	男	58	新疆	商人	小学	良好	已婚	3子1女	
冯大刚	男	45	内蒙古	农民	小学	良好	已婚	2子1女	
李秀英	女	32	吉林	工人	初中	良好	已婚	1子1女	
张国强	男	25	辽宁	干部	高中	良好	已婚	2子1女	
刘小红	女	20	黑龙江	教师	大学	良好	已婚	1子1女	
陈为民	男	55	山西	商人	小学	良好	已婚	3子1女	
赵大刚	男	42	山东	农民	小学	良好	已婚	2子1女	
孙丽娟	女	38	河北	工人	初中	良好	已婚	1子1女	
周建民	男	30	河南	干部	高中	良好	已婚	2子1女	
吴小芳	女	25	江苏	教师	大学	良好	已婚	1子1女	
郑为民	男	52	浙江	商人	小学	良好	已婚	3子1女	
冯大刚	男	40	安徽	农民	小学	良好	已婚	2子1女	
李秀英	女	35	湖北	工人	初中	良好	已婚	1子1女	
张国强	男	28	湖南	干部	高中	良好	已婚	2子1女	
刘小红	女	22	江西	教师	大学	良好	已婚	1子1女	
陈为民	男	58	四川	商人	小学	良好	已婚	3子1女	
赵大刚	男	45	广东	农民	小学	良好	已婚	2子1女	
孙丽娟	女	32	广西	工人	初中	良好	已婚	1子1女	
周建民	男	25	福建	干部	高中	良好	已婚	2子1女	
吴小芳	女	20	贵州	教师	大学	良好	已婚	1子1女	
郑为民	男	55	云南	商人	小学	良好	已婚	3子1女	
冯大刚	男	42	陕西	农民	小学	良好	已婚	2子1女	
李秀英	女	38	甘肃	工人	初中	良好	已婚	1子1女	
张国强	男	30	宁夏	干部	高中	良好	已婚	2子1女	
刘小红	女	25	青海	教师	大学	良好	已婚	1子1女	
陈为民	男	52	新疆	商人	小学	良好	已婚	3子1女	
赵大刚	男	40	内蒙古	农民	小学	良好	已婚	2子1女	
孙丽娟	女	35	吉林	工人	初中	良好	已婚	1子1女	
周建民	男	28	辽宁	干部	高中	良好	已婚	2子1女	
吴小芳	女	22	黑龙江	教师	大学	良好	已婚	1子1女	
郑为民	男	58	山西	商人	小学	良好			

ttc ttc aac aga cat tgc cag cgt gga ggt ttg ctg cag ttt gag gct 643
 Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu Gln Phe Glu Ala
 165 170 175 180

gat aaa aca gca aag gag gaa tct ctc ttc ccc gtg cca ccc agc aag 691
 Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val Pro Pro Ser Lys
 185 190 195

gag acc agt gct gag tcc caa gag tcc ttt acc atg gcc tcc tgc acc 739
 Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met Ala Ser Cys Thr
 200 205 210

tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca gag 787
 Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys Thr Glu
 215 220 225

ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct gag 835
 Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly Ala Glu
 230 235 240

acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg gag ctc 883
 Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu Glu Leu
 245 250 255 260

aat gtg ccc ttt gaa gtt ccc agc cct taa ctctaagag gtctcttggg 933
 Asn Val Pro Phe Glu Val Pro Ser Pro *
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cccctggcag ccttgcccag ttgttctctc tggactctgt tcctatacca caacagcagc 993
 aggggcctga aatgtgatgt ccacaagagc taatacccta cagatggggc atatcctatc 1053
 ccacccacc agaggattga ttctccattt cacaaggact gatctggagc atttcttgct 1113
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<213> Homo sapiens

<400> 2

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 20 25 30
 Tyr Gly Glu Gly Gly Asp Ala Tyr Cys Thr Ala Cys Pro Pro Arg Arg
 35 40 45
 Tyr Lys Ser Ser Trp Gly His His Lys Cys Gln Ser Cys Ile Thr Cys
 50 55 60
 Ala Val Ile Asn Arg Val Gln Lys Val Asn Cys Thr Ala Thr Ser Asn
 65 70 75 80
 Ala Val Cys Gly Asp Cys Leu Pro Arg Phe Tyr Arg Lys Thr Arg Ile
 85 90 95
 Gly Gly Leu Gln Asp Gln Glu Cys Ile Pro Cys Thr Lys Gln Thr Pro
 100 105 110
 Thr Ser Glu Val Gln Cys Ala Phe Gln Leu Ser Leu Val Glu Ala Asp
 115 120 125
 Ala Pro Thr Val Pro Pro Gln Glu Ala Thr Leu Val Ala Leu Val Ser
 130 135 140
 Ser Leu Leu Val Val Phe Thr Leu Ala Phe Leu Gly Leu Phe Phe Leu
 145 150 155 160
 Tyr Cys Lys Gln Phe Phe Asn Arg His Cys Gln Arg Gly Gly Leu Leu
 165 170 175
 Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
 180 185 190
 Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Glu Ser Phe Thr Met
 195 200 205
 Ala Ser Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile
 210 215 220
 Glu Cys Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr
 225 230 235 240
 Thr Gly Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp
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 Arg Leu Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
 260 265

<210> 3

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<212> DNA

<213> Artificial Sequence

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<223> degenerate sequence

<221> misc_feature

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<223> n = A,T,C or G

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tgyacngcnt	gyccnccnmg	nmgntayaar	wsnwsntggg	gncaycayaa	rtgycarwsn	180
tgyathacnt	gygcngtnat	haaymgngtn	caraargtna	aytgyacngc	nacnwsnaay	240
gcngtntgyg	gngaytgyyt	nccnmgntty	taymgnaara	cmmgnathgg	nggnytnear	300
gaycargart	gyathccntg	yacnaarc	acnccnacnw	sngargtnca	rtgygcntty	360
carytnwsny	tngtngargc	ngaygcncn	acngtncnc	cncargargc	nacnytngt	420
gcnytngtw	snwsnytnyt	ngtngtntty	acnytnngnt	tyytnngny	nttyttyytn	480
taytgyaarc	arttyttyaa	ymgncaytg	carmgngngg	gnytnytnc	rttygargcn	540
gayaaracng	cnaargarga	rwsnytnntty	ccngtncnc	cnwsnaarga	racnwsngcn	600
garwsncarg	arwsnttyac	natggcnwsn	tgyacnwsng	arwsncayws	ncaytgggt	660
caywsnccna	thgartgyac	ngarytngay	ytnccaraart	tywsnwsnws	ngcnwsntay	720
acnggngcng	aracnytnng	nggnaayacn	gtngarwsna	cnggngaymg	nytngarytn	780
aaygtncnt	tygargtncc	nwsnccn				807

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<211> 41

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<213> Artificial Sequence

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<223> Pseudo repeat motif #1

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<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(12)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (13)...(16)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (19)...(20)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (22)...(26)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
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 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (32)...(37)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (38)...(39)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (41)...(41)
 <223> Xaa is any amino acid residue

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 1 5 10 15
 Cys Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 20 25 30
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 35 40

<210> 5
 <211> 45
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Pseudo repeat motif #2

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<221> VARIANT
 <222> (3)...(15)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (16)...(17)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (19)...(20)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (22)...(23)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (24)...(24)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (26)...(33)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (34)...(36)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (38)...(44)
 <223> Each Xaa is independently any amino acid residue

<400> 5

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10					15			
Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25					30		
Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys		
			35					40					45		

<210> 6
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Pseudo repeat motif #3

<221> VARIANT
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<223> Xaa is any amino acid residue

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<222> (3)...(7)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (8)...(8)
<223> Xaa is any amino acid residue or not present

<221> VARIANT
<222> (9)...(14)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (15)...(18)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT
<222> (20)...(21)
<223> Each Xaa is independently any amino acid residue

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<222> (23)...(24)
<223> Each Xaa is independently any amino acid residue

<221> VARIANT
<222> (25)...(29)
<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (31)...(38)

<223> Each Xaa is independently any amino acid residue

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<222> (39)...(39)

<223> Xaa is any amino acid residue or not present

<221> VARIANT

<222> (41)...(47)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (49)...(49)

<223> Xaa is any amino acid residue or not present

<400> 6

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5					10						15		
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	
			20					25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys
			35				40						45			
Xaa																

<210> 7

<211> 48

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #3 alternative motif

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<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(7)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (8)...(8)

<223> Xaa is independently any amino acid residue or not present

<221> VARIANT

<222> (10)...(13)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (14)...(18)

<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT

<222> (20)...(21)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (23)...(24)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (25)...(29)

<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT

<222> (31)...(40)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (41)...(46)

<223> Each Xaa is independently any amino acid residue or not present

<221> VARIANT

<222> (48)...(48)

<223> Xaa is any amino acid residue

<400> 7

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1			5				10						15		
Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	
			20				25						30		

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
 35 40 45

<210> 8

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #4

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<222> (1)...(1)

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<221> VARIANT

<222> (3)...(12)

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<221> VARIANT

<222> (13)...(16)

<223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT

<222> (18)...(19)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (21)...(22)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (24)...(27)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (28)...(33)

<223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT

<222> (35)...(37)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (38)...(41)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (43)...(43)

<223> Each Xaa is independently any amino acid residue

<400> 8

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10						15	
Cys	Xaa	Xaa	Cys	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30		
Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa						
			35					40								

<210> 9

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Pseudo repeat motif #4 alternative motif

<221> VARIANT

<222> (1)...(1)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (3)...(12)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (13)...(16)

<223> Each Xaa is independently any amino acid residue
or not present

<221> VARIANT

<222> (18)...(22)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (24)...(27)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (28)...(33)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (34)...(37)
 <223> Each Xaa is independently any amino acid residue

<221> VARIANT
 <222> (38)...(41)
 <223> Each Xaa is independently any amino acid residue
 or not present

<221> VARIANT
 <222> (43)...(43)
 <223> Xaa is any amino acid residue

<400> 9

Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10						15		
Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20					25						30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa					
			35					40								

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<220>
 <223> oligonucleotide primer ZC25352

<400> 10
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<210> 11

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC25353

<400> 11
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<210> 12
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 <212> DNA
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<220>
 <223> oligonucleotide primer ZC25364

<400> 12
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<210> 13
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<220>
 <223> oligonucleotide primer ZC25365

<400> 13
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<210> 14
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide primer ZC25352

<400> 14
 ccttgcccag ttgttctc 18

<210> 15
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<220>
 <223> oligonucleotide primer ZC25353

<400> 15
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18

<210> 16
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 <213> Artificial protein

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 Glu Tyr Met Pro Met Glu
 1 5

<210> 17
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<220>
 <223> oligonucleotide primer ZC25598

<400> 17
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33

<210> 18
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<220>
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37

<210> 19
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 <213> Homo sapiens

<220>
 <223> tPA leader

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 tcgctcagcc aggaaatcca tgccgagttg agacgcttcc gtagatcc 108

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<220>
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 ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcattgatctc ccggaccctt 120
 gaggtcacat gcgtgggtgt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 180
 tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcggggagga gcagtacaac 240
 agcacgtacc gtgtgggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 300
 gagtacaagt gcaaggtctc caacaaagcc ctcccatcct ccatcgagaa aaccatctcc 360
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 420
 ctgaccaaga accaggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 480
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 540
 ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 600
 cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 660
 cagaagagcc tctccctgtc tccgggtaaa taa 693

<210> 21
 <211> 534
 <212> DNA
 <213> Artificial sequence

<400> 21
 atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggcgc cgtcttcgtt 60
 tcgctcagcc aggaaatcca tgccgagttg agacgcttcc gtagatccga ttgccaagaa 120
 aatgagtact gggaccaatg gggacggtgt gtcacctgcc aacggtgtgg tcctggacag 180

gagctatcca	aggattgtgg	ttatggagag	ggtggagatg	cctactgcac	agcctgccct	240
cctcgcaggt	acaaaagcag	ctggggccac	cacaaatgtc	agagttgcat	cacctgtgct	300
gtcatcaatc	gtgttcagaa	ggtcaactgc	acagctacct	ctaattgctgt	ctgtggggac	360
tgtttgccca	ggttctaccg	aaagacacgc	attggaggcc	tgcaggacca	agagtgcac	420
ccgtgcacga	agcagacccc	cacctctgag	gttcaatgtg	ccttccagtt	gagcttagtg	480
gaggcagatg	cacccacagt	ggagcccaga	tctgaatata	tgcccatgga	ataa	534

<210> 22

<211> 1200

<212> DNA

<213> Artificial Sequence

<220>

<223> construct

<400> 22

atggatgcaa	tgaagagagg	gctctgctgt	gtgctgctgc	tgtgtggcgc	cgtcttcggt	60
tcgctcagcc	aggaaatcca	tgccgagttg	agacgcttcc	gtagatccga	ttgccaagaa	120
aatgagtact	gggaccaatg	gggacggtgt	gtcacctgcc	aacgggtgtg	tcctggacag	180
gagctatcca	aggattgtgg	ttatggagag	ggtggagatg	cctactgcac	agcctgccct	240
cctcgcaggt	acaaaagcag	ctggggccac	cacaaatgtc	agagttgcat	cacctgtgct	300
gtcatcaatc	gtgttcagaa	ggtcaactgc	acagctacct	ctaattgctgt	ctgtggggac	360
tgtttgccca	ggttctaccg	aaagacacgc	attggaggcc	tgcaggacca	agagtgcac	420
ccgtgcacga	agcagacccc	cacctctgag	gttcaatgtg	ccttccagtt	gagcttagtg	480
gaggcagatg	cacccacagt	ggagcccaga	tcttcagaca	aaactcacac	atgcccaccg	540
tgcccagcac	ctgaagccga	gggggcaccg	tcagtcttcc	tcttcccccc	aaaaccecaag	600
gacaccctca	tgatctcccg	gacccttgag	gtcacatgcg	tggtggtgga	cgtgagccac	660
gaagaccctg	aggtcaagtt	caactggtac	gtggacggcg	tggaggtgca	taatgccaag	720
acaaagccgc	gggaggagca	gtacaacagc	acgtaccgtg	tggtcagcgt	cctcaccgtc	780
ctgcaccagg	actggctgaa	tggcaaggag	tacaagtgca	aggtctccaa	caaagccctc	840
ccatcctcca	tcgagaaaac	catctccaaa	gccaaagggc	agccccgaga	accacagggtg	900
tacaccctgc	ccccatcccg	ggatgagctg	accaagaacc	aggtcagcct	gacctgcctg	960
gtcaaaggct	tctatcccag	cgacatcgcc	gtggagtggg	agagcaatgg	gcagccggag	1020
aacaactaca	agaccacgcc	tcccgtgctg	gactccgacg	gctccttctt	cctctacagc	1080
aagctcaccg	tggacaagag	caggtggcag	caggggaacg	tcttctcatg	ctccgtgatg	1140
catgaggctc	tgcacaacca	ctacacgcag	aagagcctct	ccctgtctcc	gggtaaataa	1200

<210> 23

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC26463

<400> 23

atgcattaac cctcactaaa gggccttcct ggggctcttc ttcctct

47

<210> 24

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC26464

<400> 24

taatacgact cactataggg aggggcccct gctgctgttg tggat

46

<210> 25

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC26470

<400> 25

atgcattaac cctcactaaa gggacctgtg ctgtcatcaa tcgtgttca

49

<210> 26

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC26471

<400> 26

taatacgact cactataggg agggccccc aa ggtctcagct ccagtat

47

<210> 27

<211> 297

<212> PRT

<213> Homo sapiens

<400> 27

Met	Asp	Cys	Gln	Glu	Asn	Glu	Tyr	Trp	Asp	Gln	Trp	Gly	Arg	Cys	Val	1	5	10	15
Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly	20	25	30	
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg	35	40	45	
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys	50	55	60	
Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn	65	70	75	80
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile	85	90	95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro	100	105	110	
Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp	115	120	125	
Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Val	Ser	130	135	140	
Ser	Leu	Leu	Val	Val	Phe	Thr	Leu	Ala	Phe	Leu	Gly	Leu	Phe	Phe	Leu	145	150	155	160
Tyr	Cys	Lys	Gln	Phe	Phe	Asn	Arg	His	Cys	Gln	Arg	Gly	Gly	Leu	Leu	165	170	175	
Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu	Ser	Leu	Phe	Pro	Val	180	185	190	
Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln	Val	Ser	Glu	Asn	Ile	195	200	205	
Phe	Gln	Thr	Gln	Pro	Leu	Asn	Pro	Ile	Leu	Glu	Asp	Asp	Cys	Ser	Ser	210	215	220	
Thr	Ser	Gly	Phe	Pro	Thr	Gln	Glu	Ser	Phe	Thr	Met	Ala	Ser	Cys	Thr	225	230	235	240
Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	Glu	Cys	Thr	Glu	245	250	255	
Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	Thr	Gly	Ala	Glu	260	265	270	
Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	Arg	Leu	Glu	Leu	275	280	285	
Asn	Val	Pro	Phe	Glu	Val	Pro	Ser	Pro								290	295		

<210> 28
 <211> 891
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> degenerate sequence

<221> misc_feature
 <222> (1)...(891)
 <223> n = A,T,C or G

<400> 28

atggaytgyc	argaraayga	rtaytgggay	cartggggnm	gntgygtnac	ntgycarmgn	60
tgyggncng	gncargaryt	nwsnaargay	tgyggntayg	gngarggngg	ngaygcntay	120
tgyacngent	gyccnccnmg	nmgntayaar	wsnwsntggg	gncaycayaa	rtgycarwsn	180
tgyathacnt	gygcngtnat	haaymgngtn	caraargtna	aytgyacngc	nacnwsnaay	240
gcngtntgyg	gngaytgyyt	nccnmgntty	taymgnaara	cnmgnathgg	nggnytnear	300
gaycargart	gyathccntg	yacnaarcar	acnccnacnw	sngargtnca	rtgygcntty	360
carytnwsny	tngtngargc	ngaygcncn	acngtncnc	cncargargc	nacnytngt	420
gcnytngtw	snwsnytnyt	ngtngtntty	acnytnngnt	tyytnngny	nttyttyytn	480
taytgyaarc	arttyttyaa	ymgncaytgy	carmgnggng	gnytnytnc	rttygargcn	540
gayaaracng	cnaargarga	rwsnytnntty	ccngtncnc	cnwsnaarga	racnwsngcn	600
garwsncarg	tnwsngaraa	yathttycar	acncarcny	tnaayccnat	hytngargay	660
gaytgywsnw	snacnwsngg	nttyccnacc	cargarwsnt	tyacnatggc	nwsntgyacn	720
wsngarwsnc	aywsncaytg	ggtncaywsn	ccnathgart	gyacngaryt	ngayytncar	780
aarttywsnw	snwsngcnws	ntayacnggn	gcngaracny	tngngngnaa	yacngtngar	840
wsnacnggng	aymgnytna	rytnaaygt	ccnttygarg	tnccnwsncc	n	891

<210> 29
 <211> 267
 <212> PRT
 <213> Homo sapiens

<400> 29

Met	Asp	Cys	Gln	Glu	Asn	Glu	Tyr	Trp	Asp	Gln	Trp	Gly	Arg	Cys	Val
1				5				10					15		
Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly
			20				25						30		
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg
		35				40					45				
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys
50					55					60					

Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn
65					70				75					80	
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile
			85					90						95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro
		100					105						110		
Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp
	115					120					125				
Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Gly	Gly
	130					135					140				
Leu	Leu	Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu	Ser	Leu	Phe
145				150					155					160	
Pro	Val	Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln	Val	Ser	Glu
				165				170						175	
Asn	Ile	Phe	Gln	Thr	Gln	Pro	Leu	Asn	Pro	Ile	Leu	Glu	Asp	Asp	Cys
			180				185						190		
Ser	Ser	Thr	Ser	Gly	Phe	Pro	Thr	Gln	Glu	Ser	Phe	Thr	Met	Ala	Ser
	195					200						205			
Cys	Thr	Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	Glu	Cys
	210					215					220				
Thr	Glu	Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	Thr	Gly
225					230					235				240	
Ala	Glu	Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	Arg	Leu
				245				250						255	
Glu	Leu	Asn	Val	Pro	Phe	Glu	Val	Pro	Ser	Pro					
		260					265								

<210> 30

<211> 801

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate sequence

<221> misc_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 30

atggaytgyc	argaraayga	rtaytggg	ay cartgggg	nm gntgygtnac	ntgycarmgn	60
tgyggncng	gncargaryt	nwsnaargay	tgyggntayg	gngarggngg	ngaygcntay	120
tgyacngcnt	gyccnccnmg	nmgntayaar	wsnwsntggg	gncaycayaa	rtgycarwsn	180

tgyathacnt	gygcngtnat	haaymgngtn	caraargtna	aytgyacngc	nacnwsnaay	240
gcngtntgyg	gngaytgyyt	nccnmgnatty	taymgnaara	cnmgnathgg	nggnytnear	300
gaycargart	gyathccntg	yacnaarcar	acnccnacnw	sngargtnca	rtgygcntty	360
carytnwsny	tngtngargc	ngaygcncn	acngtncnc	cncargargc	nacnytngt	420
gcnytnngng	gnytnytnc	rttygargcn	gayaaracng	cnaargarga	rwsnytnnty	480
ccngtncnc	cnwsnaarga	racnwsngcn	garwsncarg	tnwsngaraa	yathttycar	540
acncarccny	tnaayccnat	hytngargay	gaytgywsnw	snacnwsngg	nttyccnacn	600
cargarwsnt	tyacnatggc	nwsntgyacn	wsngarwsnc	aywsncaytg	ggtncaywsn	660
ccnathgart	gyacngaryt	ngayytncar	aarttywsnw	snwsngcnws	ntayacnggn	720
gcngaracny	tngnggnaa	yacngtngar	wsnacngng	aymgnytna	rytnaaygt	780
ccnttygarg	tnccnwsncc	n				801

<210> 31
 <211> 529
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(529)
 <223> n = A,T,C or G

ggattcnatn	nctgaggntg	natggcnttc	nagttnwgas	tkagtggagg	cagatgcasc	60
cacagtgcc	gcctcaggag	gycacacttg	ttgcrmtggt	gagcagcstg	ctagtgggtg	120
ttrccctggc	cttctgagg	ctcttcttc	tcwacygcaa	gcagttcttc	aacagacatt	180
gycagcsng	gaggtttgct	gcagtttgag	gctgatraaa	cagcaaagga	ggaatctstm	240
ttycycgtgc	cacccagcaa	ggagaccagt	gctgagtccc	aagtgagtga	gaacatyttt	300
cakacccagm	cacttaaccc	tatcctyrag	gacgactgca	rtctgactag	tggyttcccc	360
acacaggart	metttaccat	ggcctyctgc	acctyagaga	gccactscca	ctgggwccac	420
arcccatcg	aatgcacaka	gctggacctg	caaaagtttt	ccagctctgc	ctctataact	480
ggagctgara	ccttgggggg	aaacacagnc	aaaagcactg	ganacaggg		529

<210> 32
 <211> 401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(401)
 <223> n = A,T,C or G

<400> 32

cagttgagct	tagtggaggc	agatgcaccc	acagtgcacc	ctcaggaggc	cacacttggt	60
gsactggagg	tttgctgcag	tttgaggctg	ataaaacagc	aaaggaggaa	tctctcttns	120
ccgtgccacc	cagcaaggag	accagtgcgt	agtcccaagt	gagtgagaac	atctttcaga	180
cccagccact	taaccctatc	ctcgaggacg	actgcagctc	gactagtggc	ttccccacac	240
aggagtcctt	taccatggcc	tcctgcacct	cagagagcca	ctcccactgg	gtccacagcc	300
ccatcgaatg	cacagagctg	gacctgcaaa	agttttccag	ctctgcctcc	tatactggag	360
ctgagacctt	ggggggaaac	acagtcgaaa	gcactggaga	c		401

<210> 33

<211> 528

<212> DNA

<213> Homo sapiens

<400> 33

ctctgagggt	caatgtgcct	tccagttgag	cttagtggag	gcagatgcac	ccacagtgcc	60
ccctcaggag	gccacacttg	ttgcactggg	gagcagcctg	ctagtgggtg	ttaccctggc	120
cttcctgggg	ctcttcttcc	tctactgcaa	gcagttcttc	aacagacatt	gccagcgtgt	180
tgcaggaggt	ttgctgcagt	ttgaggctga	taaaacagca	aaggagggaat	ctctcttccc	240
cgtgccaccc	agcaaggaga	ccagtgcctg	gtcccaagtg	agtgagaaca	tctttcagac	300
ccagccactt	aaccctatcc	tcgaggacga	ctgcagctcg	actagtggct	tccccacaca	360
ggagtccttt	accatggcct	cctgcacctc	agagagccac	tcccactggg	tccacagccc	420
catcgaatgc	acagagctgg	acctgcaaaa	gttttccagc	tctgcctcct	atactggagc	480
tgagaccttg	gggggaaaca	cagtcgaaag	cactggagac	aggctgga		528

<210> 34

<211> 175

<212> PRT

<213> Homo sapiens

<400> 34

Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp	Ala
1				5				10						15	
Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Val	Ser	Ser
			20					25						30	
Leu	Leu	Val	Val	Phe	Thr	Leu	Ala	Phe	Leu	Gly	Leu	Phe	Phe	Leu	Tyr
			35				40							45	
Cys	Lys	Gln	Phe	Phe	Asn	Arg	His	Cys	Gln	Arg	Val	Ala	Gly	Gly	Leu
			50			55					60				
Leu	Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu	Ser	Leu	Phe	Pro
65					70				75					80	
Val	Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln	Val	Ser	Glu	Asn
			85					90						95	

Ile	Phe	Gln	Thr	Gln	Pro	Leu	Asn	Pro	Ile	Leu	Glu	Asp	Asp	Cys	Ser
		100						105					110		
Ser	Thr	Ser	Gly	Phe	Pro	Thr	Gln	Glu	Ser	Phe	Thr	Met	Ala	Ser	Cys
		115					120					125			
Thr	Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	Glu	Cys	Thr
		130				135					140				
Glu	Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	Thr	Gly	Ala
145					150					155					160
Glu	Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	Arg	Leu	
			165					170						175	

<210> 35

<211> 299

<212> PRT

<213> Homo sapiens

<400> 35

Met	Asp	Cys	Gln	Glu	Asn	Glu	Tyr	Trp	Asp	Gln	Trp	Gly	Arg	Cys	Val
1				5					10					15	
Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly
		20					25						30		
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg
	35					40					45				
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys
	50				55					60					
Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn
65				70					75						80
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile
			85					90						95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro
		100					105						110		
Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp
	115					120						125			
Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Val	Ser
	130					135					140				
Ser	Leu	Leu	Val	Val	Phe	Thr	Leu	Ala	Phe	Leu	Gly	Leu	Phe	Phe	Leu
145				150					155						160
Tyr	Cys	Lys	Gln	Phe	Phe	Asn	Arg	His	Cys	Gln	Arg	Val	Ala	Gly	Gly
			165					170						175	
Leu	Leu	Gln	Phe	Glu	Ala	Asp	Lys	Thr	Ala	Lys	Glu	Glu	Ser	Leu	Phe
		180						185					190		
Pro	Val	Pro	Pro	Ser	Lys	Glu	Thr	Ser	Ala	Glu	Ser	Gln	Val	Ser	Glu
	195						200						205		

Asn Ile Phe Gln Thr Gln Pro Leu Asn Pro Ile Leu Glu Asp Asp Cys
 210 215 220
 Ser Ser Thr Ser Gly Phe Pro Thr Gln Glu Ser Phe Thr Met Ala Ser
 225 230 235 240
 Cys Thr Ser Glu Ser His Ser His Trp Val His Ser Pro Ile Glu Cys
 245 250 255
 Thr Glu Leu Asp Leu Gln Lys Phe Ser Ser Ser Ala Ser Tyr Thr Gly
 260 265 270
 Ala Glu Thr Leu Gly Gly Asn Thr Val Glu Ser Thr Gly Asp Arg Leu
 275 280 285
 Glu Leu Asn Val Pro Phe Glu Val Pro Ser Pro
 290 295

<210> 36
 <211> 431
 <212> DNA
 <213> Homo sapiens

<400> 36
 ctc tga ggt tca atg tgc ctt cca gtt gag ctt agt gga ggc aga tgc 48
 acc cac agt gcc ccc tca gga ggc cac act tgt tgc act gga ggt ttg 96
 ctg cag ttt gag gct gat aaa aca gca aag gag gaa tct ctc ttc ccc 144
 gtg cca ccc agc aag gag acc agt gct gag tcc caa gtg agt gag aac 192
 atc ttt cag acc cag cca ctt aac cct atc ctc gag gac gac tgc agc 240
 tcg act agt ggc ttc ccc aca cag gag tcc ttt acc atg gcc tcc tgc 288
 acc tca gag agc cac tcc cac tgg gtc cac agc ccc atc gaa tgc aca 336
 gag ctg gac ctg caa aag ttt tcc agc tct gcc tcc tat act gga gct 384
 gag acc ttg ggg gga aac aca gtc gaa agc act gga gac agg ctg ga 431

<210> 37
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 37
 Leu Gly Ser Met Cys Leu Pro Val Glu Leu Ser Gly Gly Arg Cys Thr
 1 5 10 15
 His Ser Ala Pro Ser Gly Gly His Thr Cys Cys Thr Gly Gly Leu Leu
 20 25 30
 Gln Phe Glu Ala Asp Lys Thr Ala Lys Glu Glu Ser Leu Phe Pro Val
 35 40 45
 Pro Pro Ser Lys Glu Thr Ser Ala Glu Ser Gln Val Ser Glu Asn Ile
 50 55 60

Phe	Gln	Thr	Gln	Pro	Leu	Asn	Pro	Ile	Leu	Glu	Asp	Asp	Cys	Ser	Ser
65					70					75					80
Thr	Ser	Gly	Phe	Pro	Thr	Gln	Glu	Ser	Phe	Thr	Met	Ala	Ser	Cys	Thr
				85					90					95	
Ser	Glu	Ser	His	Ser	His	Trp	Val	His	Ser	Pro	Ile	Glu	Cys	Thr	Glu
			100					105					110		
Leu	Asp	Leu	Gln	Lys	Phe	Ser	Ser	Ser	Ala	Ser	Tyr	Thr	Gly	Ala	Glu
		115					120					125			
Thr	Leu	Gly	Gly	Asn	Thr	Val	Glu	Ser	Thr	Gly	Asp	Arg	Leu		
	130					135					140				

<210> 38

<211> 173

<212> PRT

<213> Homo sapiens

<400> 38

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Thr	Cys	Gln	Arg	Cys	Gly	Pro	Gly	Gln	Glu	Leu	Ser	Lys	Asp	Cys	Gly
			20					25					30		
Tyr	Gly	Glu	Gly	Gly	Asp	Ala	Tyr	Cys	Thr	Ala	Cys	Pro	Pro	Arg	Arg
		35					40					45			
Tyr	Lys	Ser	Ser	Trp	Gly	His	His	Lys	Cys	Gln	Ser	Cys	Ile	Thr	Cys
	50					55					60				
Ala	Val	Ile	Asn	Arg	Val	Gln	Lys	Val	Asn	Cys	Thr	Ala	Thr	Ser	Asn
65					70					75					80
Ala	Val	Cys	Gly	Asp	Cys	Leu	Pro	Arg	Phe	Tyr	Arg	Lys	Thr	Arg	Ile
				85					90					95	
Gly	Gly	Leu	Gln	Asp	Gln	Glu	Cys	Ile	Pro	Cys	Thr	Lys	Gln	Thr	Pro
		100						105					110		
Thr	Ser	Glu	Val	Gln	Cys	Ala	Phe	Gln	Leu	Ser	Leu	Val	Glu	Ala	Asp
		115					120					125			
Ala	Pro	Thr	Val	Pro	Pro	Gln	Glu	Ala	Thr	Leu	Val	Ala	Leu	Glu	Val
	130					135					140				
Cys	Cys	Ser	Leu	Arg	Leu	Ile	Lys	Gln	Gln	Arg	Arg	Asn	Leu	Ser	Ser
145					150					155					160
Pro	Cys	His	Pro	Ala	Arg	Arg	Pro	Val	Leu	Ser	Pro	Lys			
				165					170						

<210> 39

<211> 519

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate polynucleotide sequence

<221> misc_feature

<222> (1)...(519)

<223> n = A,T,C or G

<400> 39

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tgyacngent gyccnccnmg nmgtayaar wsnwsntggg gncaycayaa rtgycarwsn	180
tgyathacnt gygcngtnat haaymgngtn caraargtna aytgyacngc nacnwsnaay	240
gcngtntgyg gngaytgyyt nccnmgtty taymgnaara cnmgnathgg nggnytnear	300
gaycargart gyathccntg yacnaarcac acnccnacnw sngargtnca rtgygcntty	360
carytnwsny tngtngargc ngaygcncn acngtncnc cncargargc nacnytnngtn	420
gcnytnarg tntgytgyws nytnmgnytn athaarcac armgnmgnaa yytnwsnwsn	480
ccntgycayc cngcnmgmng nccngtnytn wsncnaar	519

<210> 40

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide ZC26463

<400> 40

atgcattaac cctcactaaa ggccttcct ggggctcttc ttctct	47
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<210> 41

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide sequence ZC 26464

<400> 41

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<210> 42

<211> 49
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<220>
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<400> 42
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<210> 43
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide sequence ZC 26471

<400> 43
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<210> 44
 <211> 657
 <212> DNA
 <213> murine

<400> 44
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 agagatgccca aggtgcctca tgtgcctgat gagaaatccc aggatgcagt aggccttgag 180
 cagcagcacc tgttgaccac agcaccagct tccagcagca gctccctaga gagctcagcc 240
 agcgctgggg accgaagggc gccccttggg ggccatcccc aagcaagagt catggcggag 300
 gcccaagggg ttcaggaggc ccgtgccagc tccaggattt cagattcttc ccacggaagc 360
 cacgggaccc acgtcaacgt cacctgcacg gtgaacgtct gtagcagctc tgaccacagt 420
 tctcagtgtc ctcccaagc cagcgccaca gtgggagacc cagatgccaa gccctcagcg 480
 tccccaaagg atgagcaggt ccccttctct caggaggagt gtccgtctca gtccccgtgt 540
 gagactacag agacactgca gagccatgag aagcccttgc cccttggtgt gccggatatg 600
 ggcatgaagc ccagccaagc tggctgggtt gatcagattg cagtcaaagt ggcctga 657

<210> 45
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 <212> DNA

<213> Artificial Sequence

<220>

<223> artificial cDNA sequence

<400> 45

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accttcccgt	aatccctcc	ccttcccgga	attacacacg	cgtatttccc	agaaaaggaa	180
ctgtagattt	ctaggaattc	aatccttggc	cacgcgttta	caccggaagt	tttccatatt	240
aggaattcct	tccggtttcc	tttctcgagg	ccaccgtggt	tgagcccgac	actcattcat	300
aaaacgcttg	ttataaaagc	agtggctgcg	gcgccttcgt	actccaaccg	catctgcagc	360
gagcaactga	gaagccaagg	atccaggctg	aattcatggg	tctcaacccc	cagctagttg	420
tcatacctgct	cttctttctc	gaatgtacca	ggagccatat	ccacggatgc	gacaaaaatc	480
acttgagaga	gatcatcggc	attttgaacg	aggtcacagg	agaagggacg	ccatgcacgg	540
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gtagggcttc	caaggtgctt	cgcataatctt	attttaaaca	tgggaaaact	ccatgcttga	660
agaagaactc	tagtgttctc	atggagctgc	agagactctt	tcgggctttt	cgatgcctgg	720
attcatcgat	aagctgcacc	atgaatgagt	ccaagtccac	atcactgaaa	gacttcctgg	780
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<210> 46

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide sequence ZC28835

<400> 46

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<210> 47

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide sequence ZC 28836

<400> 47

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<210> 48

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC 28830

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29

<210> 49

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC 28837

<400> 49

gctctagagg ggtcaggcca ctttgactg

29

<210> 50

<211> 1081

<212> DNA

<213> Artificial Sequence

<220>

<223> DNA construct

<400> 50

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tgcacagcct	gccctcctcg	caggtacaaa	agcagctggg	gccaccacaa	atgtcagagt	180
tgcatacct	gtgctgtcat	caatcgtggt	cagaaggtea	actgcacagc	tacctctaat	240
gctgtctgtg	gggactgttt	gcccagggtc	taccgaaaga	cacgcattgg	aggcctgcag	300
gaccaagagt	gcatcccgtg	cacgaagcag	acccccacct	ctgagggttc	atgtgccttc	360
cagttgagct	tagtggaggc	agatgcaccc	acagtgcacc	ctcaggaggt	caccgttggc	420
atctctcttc	caattggtct	gattgttgga	gtgacatcac	tgggtctgct	gatgttagga	480
ctggatgaact	gcatcatcct	ggtgcagagg	aaaaagaagc	cctcctgcct	acaaagagat	540
gccaaagggtgc	ctcatgtgcc	tgatgagaaa	tcccaggatg	cagtaggcct	tgagcagcag	600

姓名	性别	年龄	籍贯	职业	文化程度	健康状况	婚姻状况	子女情况	其他
王德胜	男	45	山东	工人	小学	良好	已婚	2子1女	
李秀英	女	38	河北	农民	初中	良好	已婚	1子1女	
张国强	男	52	河南	干部	高中	良好	已婚	2子1女	
刘小红	女	28	江苏	教师	大学	良好	未婚	无	
陈为民	男	60	浙江	退休	小学	一般	已婚	3子2女	
赵大刚	男	35	湖北	工人	初中	良好	已婚	1子1女	
孙丽娟	女	42	湖南	农民	小学	良好	已婚	2子1女	
周建民	男	55	四川	干部	高中	良好	已婚	2子1女	
吴小芳	女	32	广东	教师	大学	良好	未婚	无	
郑为民	男	48	广西	工人	初中	良好	已婚	1子1女	
冯大刚	男	58	福建	退休	小学	一般	已婚	3子2女	
李秀英	女	38	河北	农民	初中	良好	已婚	1子1女	
张国强	男	52	河南	干部	高中	良好	已婚	2子1女	
刘小红	女	28	江苏	教师	大学	良好	未婚	无	
陈为民	男	60	浙江	退休	小学	一般	已婚	3子2女	
赵大刚	男	35	湖北	工人	初中	良好	已婚	1子1女	
孙丽娟	女	42	湖南	农民	小学	良好	已婚	2子1女	
周建民	男	55	四川	干部	高中	良好	已婚	2子1女	
吴小芳	女	32	广东	教师	大学	良好	未婚	无	
郑为民	男	48	广西	工人	初中	良好	已婚	1子1女	
冯大刚	男	58	福建	退休	小学	一般	已婚	3子2女	